

Abcg1 Cas9-CKO Strategy

Designer:

Daohua Xu

Reviewer:

Huimin Su

Design Date:

2019-9-28

Project Overview

Project Name

Abcg1

Project type

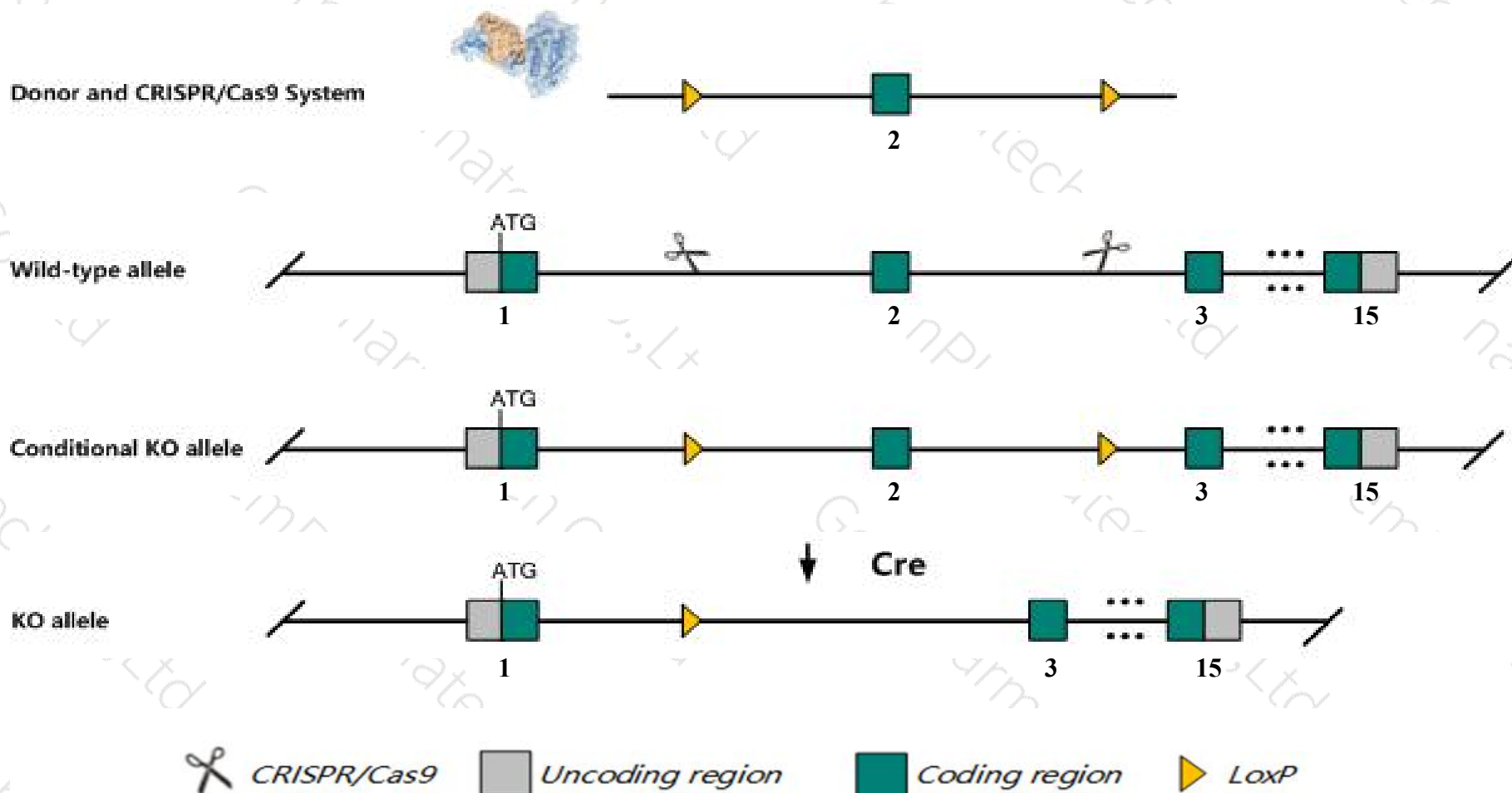
Cas9-CKO

Strain background

C57BL/6JGpt

Conditional Knockout strategy

This model will use CRISPR/Cas9 technology to edit the *Abcg1* gene. The schematic diagram is as follows:



Technical routes

- The *Abcg1* gene has 5 transcripts. According to the structure of *Abcg1* gene, exon2 of *Abcg1-201* (ENSMUST00000024829.7) transcript is recommended as the knockout region. The region contains 244bp coding sequence. Knock out the region will result in disruption of protein function.
- In this project we use CRISPR/Cas9 technology to modify *Abcg1* gene. The brief process is as follows: CRISPR/Cas9 system and Donor were microinjected into the fertilized eggs of C57BL/6JGpt mice. Fertilized eggs were transplanted to obtain positive F0 mice which were confirmed by PCR and sequencing. A stable F1 generation mouse model was obtained by mating positive F0 generation mice with C57BL/6JGpt mice.
- The flox mice will be knocked out after mating with mice expressing Cre recombinase, resulting in the loss of function of the target gene in specific tissues and cell types.

- According to the existing MGI data, Mice homozygous for a knock-out allele exhibit abnormal lipid homeostasis, increased numbers of multiple immune cell types, and abnormal response to a high fat diet.
- The *Abcg1* gene is located on the Chr17. If the knockout mice are crossed with other mice strains to obtain double gene positive homozygous mouse offspring, please avoid the two genes on the same chromosome.
- This Strategy is designed based on genetic information in existing databases. Due to the complexity of biological processes, all risk of loxp insertion on gene transcription, RNA splicing and protein translation cannot be predicted at existing technological level.

Gene information (NCBI)

Abcg1 ATP binding cassette subfamily G member 1 [*Mus musculus* (house mouse)]






Gene ID: 11307, updated on 12-Aug-2019

Summary

Official Symbol	Abcg1 provided by MGI
Official Full Name	ATP binding cassette subfamily G member 1 provided by MGI
Primary source	MGI:MGI:107704
See related	Ensembl:ENSMUSG00000024030
Gene type	protein coding
RefSeq status	REVIEWED
Organism	Mus musculus
Lineage	Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi; Mammalia; Eutheria; Euarchontoglires; Glires; Rodentia; Myomorpha; Muroidea; Muridae; Murinae; Mus; Mus
Also known as	Abc8; White; AW413978
Summary	The protein encoded by this gene is a member of the superfamily of ATP-binding cassette (ABC) transporters. ABC proteins transport various molecules across extra- and intra-cellular membranes. ABC genes are divided into seven distinct subfamilies (ABC1, MDR/TAP, MRP, ALD, OABP, GCN20, White). This protein is a member of the White subfamily. The human protein is involved in macrophage cholesterol efflux and may regulate cellular lipid homeostasis in other cell types. [provided by RefSeq, Jul 2008]
Expression	Broad expression in thymus adult (RPKM 31.5), lung adult (RPKM 23.3) and 16 other tissues See more
Orthologs	human all

Transcript information (Ensembl)

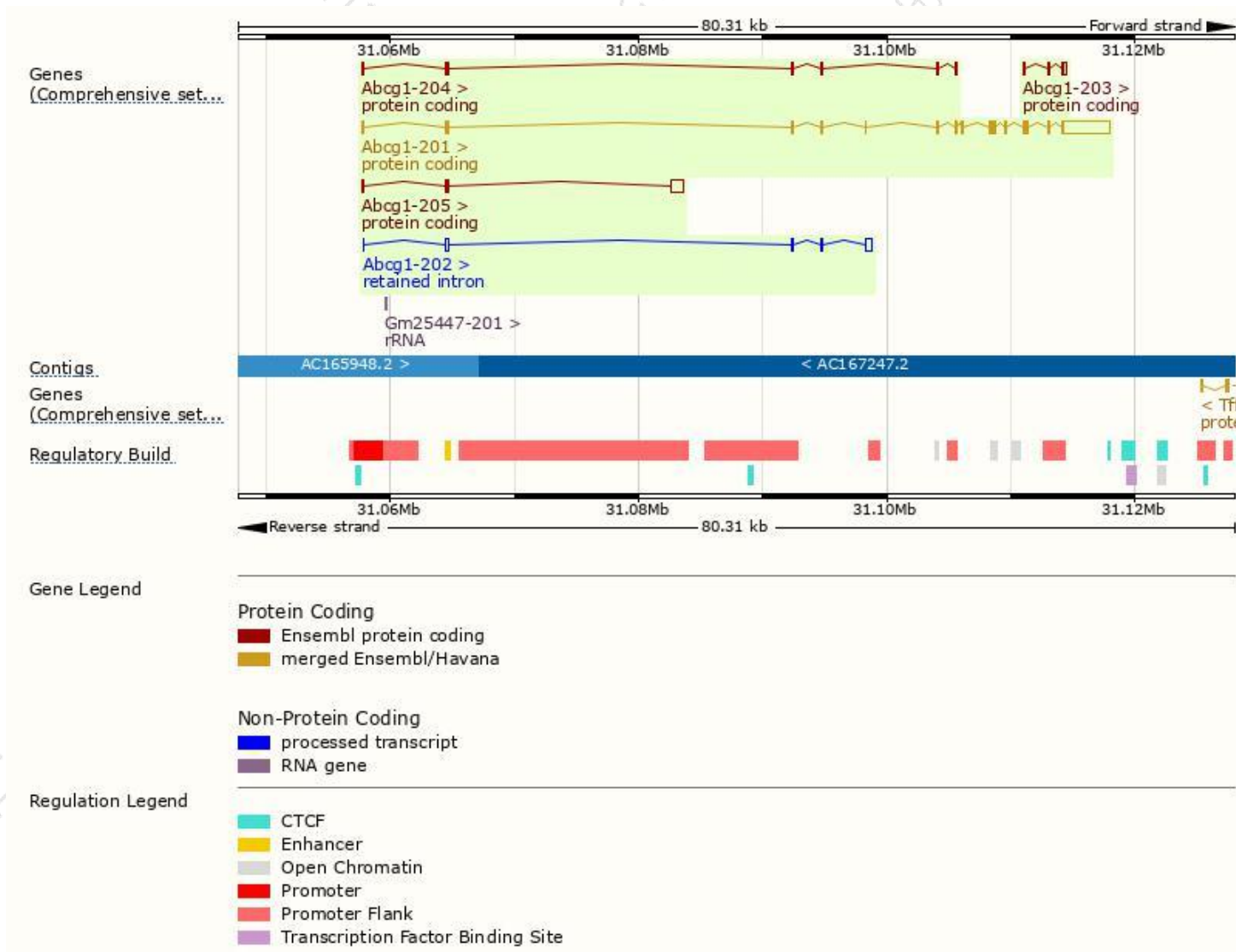
The gene has 5 transcripts,all transcripts are shown below:

Name	Transcript ID	bp	Protein	Biotype	CCDS	UniProt	Flags
Abcg1-201	ENSMUST00000024829.7	5832	666aa	 Protein coding	CCDS28602	Q0VDW9 Q64343	TSL:1 GENCODE basic APPRIS P1
Abcg1-205	ENSMUST00000236427.1	1372	104aa	 Protein coding	-	A0A494B9K1	GENCODE basic
Abcg1-204	ENSMUST00000236391.1	912	257aa	 Protein coding	-	A0A494B9N8	CDS 3' incomplete
Abcg1-203	ENSMUST00000236241.1	644	146aa	 Protein coding	-	A0A494BA50	CDS 5' incomplete
Abcg1-202	ENSMUST00000139013.1	1085	No protein	 Retained intron	-	-	TSL:1

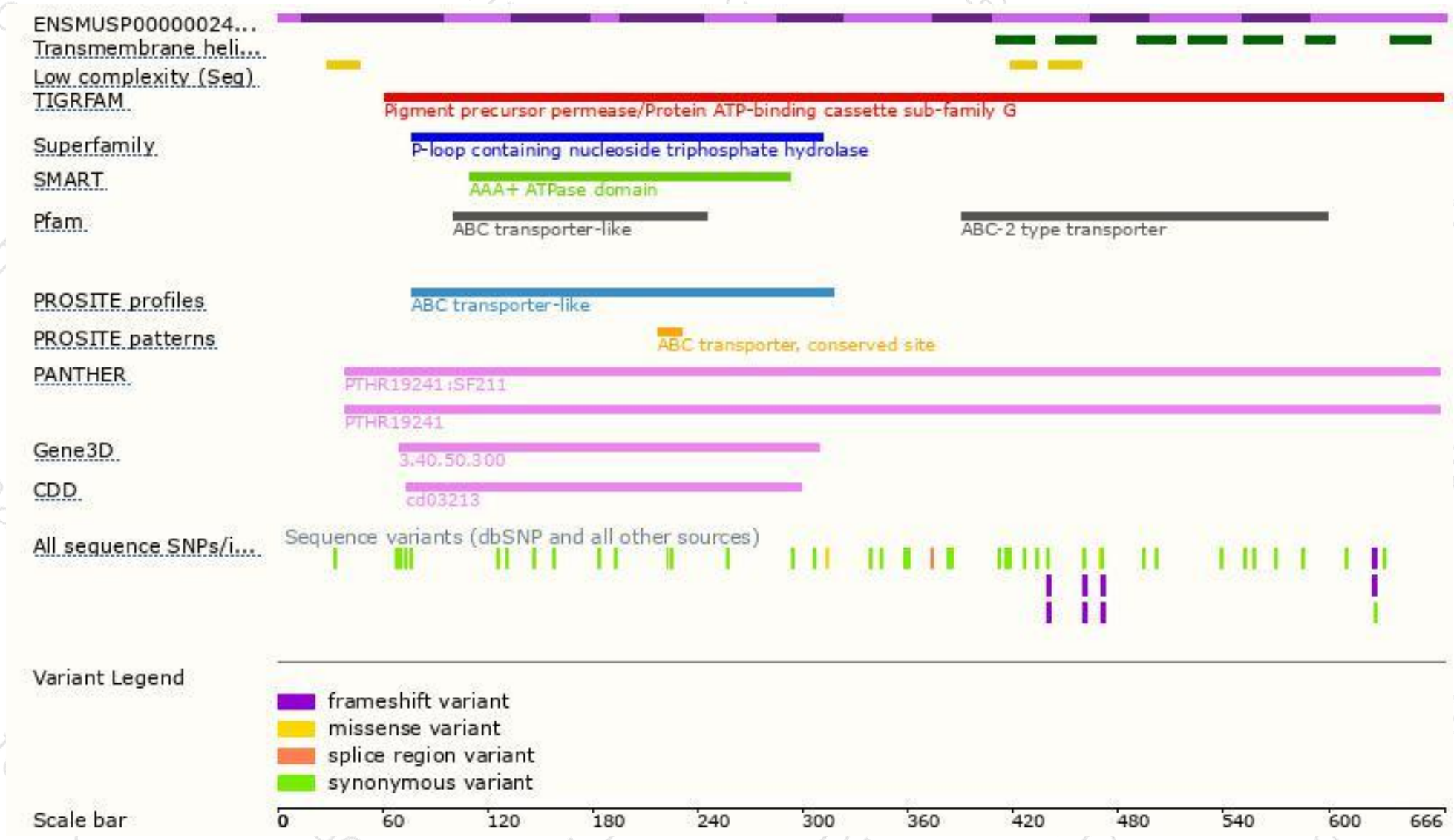
The strategy is based on the design of *Abcg1-201* transcript,The transcription is shown below



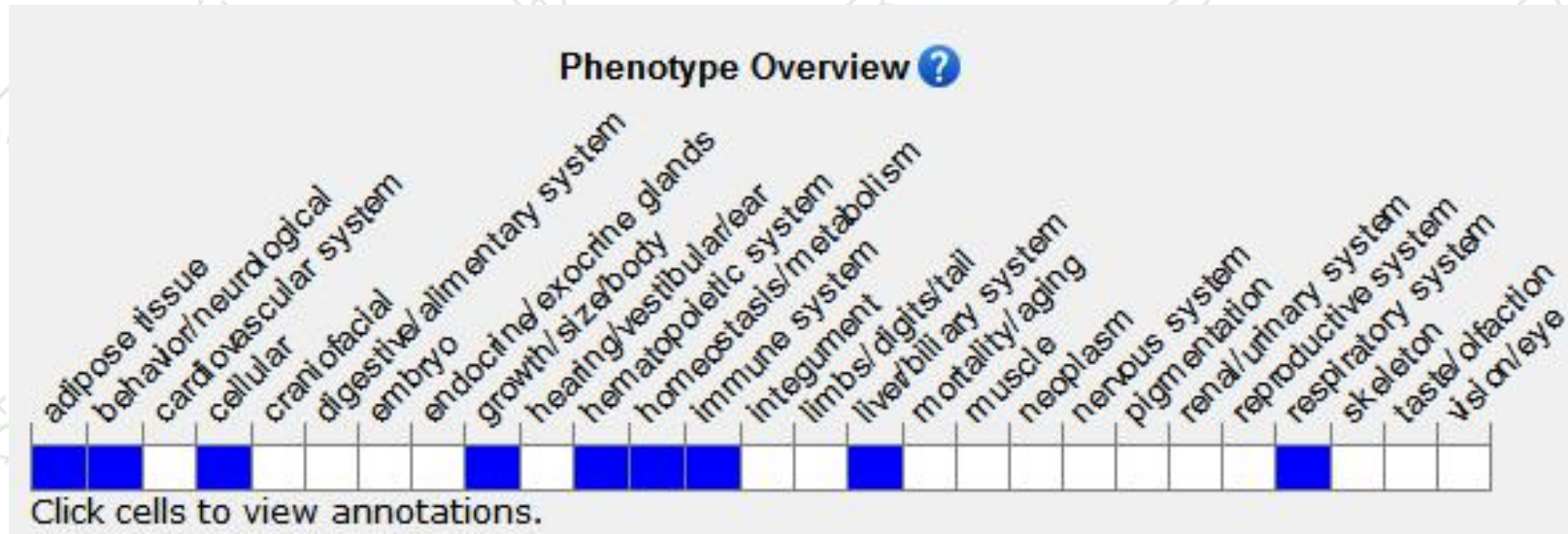
Genomic location distribution



Protein domain



Mouse phenotype description(MGI)



Phenotypes affected by the gene are marked in blue. Data quoted from MGI database(<http://www.informatics.jax.org/>).

According to the existing MGI data, Mice homozygous for a knock-out allele exhibit abnormal lipid homeostasis, increased numbers of multiple immune cell types, and abnormal response to a high fat diet.

If you have any questions, you are welcome to inquire.

Tel: 400-9660890

